DANIEL SHRINER, Ph.D.

CONTACT INFORMATION

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CITIZENSHIP

United States of America

EDUCATION

2003   Ph.D., Department of Microbiology, University of Washington, Seattle, WA
Thesis: "Population genetics of human immunodeficiency virus type 1 during within-host chronic infection"

1995   B.S., Department of Microbiology, University of Maryland, College Park, MD
Graduated summa cum laude

CONTINUING EDUCATION

2009:   The Dark Matter of Genomic Associations with Complex Diseases: Explaining the Unexplained Heritability from Genome-wide Association Studies, February 2–3, 2009, National Human Genome Research Institute, National Institutes of Health, MD

2007:   Introduction to Human Population Genetics Theory, August 23–December 4, 2007, University of Alabama at Birmingham, Birmingham, AL

2007:   Modeling, Networks and Evolution of Complex Systems, June 18–22, 2007, New England Complex Systems Institute, Cambridge, MA

2007:   Statistical Genetics II, January 8–April 26, 2007, University of Alabama at Birmingham, Birmingham, AL

2007:   Complex Physical, Biological & Social Systems, January 8–12, 2007, New England Complex Systems Institute, Cambridge, MA

2006:   Bayesian Data Analysis, August 22–November 28, 2006, University of Alabama at Birmingham, Birmingham, AL

2006:   Statistics, Images, and Perceptions of Truth: Detecting Research Bias and Misconduct, September 14–15, 2006, University of Alabama at Birmingham, Birmingham, AL

2006:   Statistical Bioinformatics, June 1–August 1, 2006, University of Alabama at Birmingham, Birmingham, AL

2006:   R Fundamentals and Programming Techniques, February 27–28, 2006, University of Alabama at Birmingham, Birmingham, AL

2005:   Advanced Gene Mapping/Linkage Course, December 12–16, 2005, Rockefeller University, New York, NY
- Awarded travel stipend

2005:   Missing Data, August 4–5, 2005, University of Alabama at Birmingham, Birmingham, AL

2005:   5th Annual National Institute of Diabetes & Digestive & Kidney Diseases Short Course on Statistical Genetics, May 16–19, 2005, University of Alabama at Birmingham, Birmingham, AL

EXPERIENCE

2008–present   Research Fellow, Center for Research on Genomics and Global Health, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD
Supervisor: Dr. Charles Rotimi

2005–2008   Postdoctoral Scholar, University of Alabama at Birmingham, Birmingham, AL
Advisors: Drs. David B. Allison and Nengjun Yi

2004–2005   Postdoctoral Fellow, University of Washington, Seattle, WA
Advisor: Dr. John E. Mittler

2003–2004   Postdoctoral Fellow, University of Washington, Seattle, WA
Advisor: Dr. James I. Mullins

1996–2003   Research Assistant, University of Washington, Seattle, WA
Advisor: Dr. James I. Mullins

1995–1996   Teaching Assistant, University of Washington, Seattle, WA
- MICROM 411: Gene Action
- MICROM 302: General Microbiology Laboratory

1993–1995   Undergraduate Research Assistant, University of Maryland, College Park, MD
Senior thesis: "Recombination in the human immunodeficiency virus: analysis *in vitro* of the influence of specific nucleotide sequences on reverse transcriptase catalyzed recombination"

PUBLICATIONS
Articles and Letters

- DeStefano, J. J., Roberts, B., and *Shriner, D*. 1997. The mechanism of retroviral recombination: the role of sequences proximal to the point of strand transfer. *Arch. Virol.* 142(9): 1797–1812.
- Liu, S.-L., Schacker, T., Musey, L., *Shriner, D.*, McElrath, M. J., Corey, L., and Mullins, J. I. 1997. Divergent patterns of progression to AIDS after infection from the same source: human immunodeficiency virus type 1 evolution and antiviral responses. *J. Virol.* 71(6): 4284–4295.
- Liu, S.-L., Mittler, J. E., Nickle, D. C., Mulvania, T. M., *Shriner, D.*, Rodrigo, A. G., Kosloff, B., He, X., Corey, L., and Mullins, J. I. 2002. Selection for human immunodeficiency virus type 1 recombinants in a patient with rapid progression to AIDS. *J. Virol.* **76(21)**: 10674–10684.
- Nickle, D. C., Jensen, M. A., Gottlieb, G. S., *Shriner, D.*, Learn, G. H., Rodrigo, A. G., and Mullins, J. I. 2003. Consensus and ancestral state HIV vaccines. *Science*. **299(5612)**: 1515–1517.
- *Shriner, D.*, Nickle, D. C., Jensen, M. A., and Mullins, J. I. 2003. Potential impact of recombination on sitewise approaches for detecting positive natural selection. *Genet. Res.* **81(2)**: 115–121.
- Nickle, D. C., *Shriner, D.,* Mittler, J. E., Frenkel, L. M., and Mullins, J. I. 2003. Importance and detection of virus reservoirs and compartments of HIV infection. *Curr. Opin. Microbiol.* **6(4)**: 410–416.
- Nickle, D. C., Jensen, M. A., *Shriner, D.*, Brodie, S. J., Frenkel, L. M., Mittler, J. E., and Mullins, J. I. 2003. Evolutionary indicators of human immunodeficiency virus type 1 reservoirs and compartments. *J. Virol.* **77(9)**: 5540–5546.
- Jensen, M. A., Li, F.-S., van 't Wout, A. B., Nickle, D. C., *Shriner, D.*, He, H.-X., McLaughlin, S., Shankarappa, R., Margolick, J. B., and Mullins, J. I. 2003. Improved coreceptor usage prediction and genotypic monitoring of R5-to-X4 transition by motif analysis of human immunodeficiency virus type 1 *env* V3 loop sequences. *J. Virol.* **77(24)**: 13376–13388.
- *Shriner, D.*, Shankarappa, R., Jensen, M. A., Nickle, D. C., Mittler, J. E., Margolick, J. B., and Mullins, J. I. 2004. Influence of random genetic drift on HIV-1 *env* evolution during chronic infection. *Genetics* **166(3)**: 1155–1164.
- *Shriner, D.*, Rodrigo, A. G., Nickle, D. C., and Mullins, J. I. 2004. Pervasive genomic recombination of HIV-1 *in vivo*. *Genetics* **167(4)**: 1573–1583.
- Liu, Y., Nickle, D. C., *Shriner, D.*, Jensen, M. A., Learn, G. H., Jr., Mittler, J. E., and Mullins, J. I. 2004. Molecular clock-like evolution of human immunodeficiency virus type 1. *Virology* **329(1)**: 101-108.
- *Shriner, D.*, Liu, Y., Nickle, D. C., and Mullins, J. I. 2006. Evolution of intrahost HIV-1 genetic diversity during chronic infection. *Evolution* **60(6)**: 1165–1176.
- Liu, Y., McNevin, J., Cao, J., Zhao, H., Genowati, I., Wong, K., McLaughlin, S., McSweyn, M. D., Diem, K., Stevens, C. E., Maenza, J., He, H., Nickle, D. C., *Shriner, D.*, Holte, S. E., Collier, A. C., Corey, L., McElrath, M. J., and Mullins, J. I. 2006. Selection on the HIV-1 proteome following primary infection. *J. Virol.* **80(19)**: 9519–9529.
- Musani, S. K., *Shriner, D.*, Liu, N., Feng, R., Coffey, C. S., Yi, N., Tiwari, H. K., and Allison, D. B. 2007. Detection of gene × gene interactions in genome-wide association studies of human population data. *Hum. Hered.* **63(2)**: 67–84.
- Yandell, B. S., Mehta, T., Banerjee, S., *Shriner, D.*, Venkataraman, R., Moon, J. Y., Neely, W. W., Wu, H., von Smith, R., and Yi, N. 2007. R/qtlbim: QTL with Bayesian interval mapping in experimental crosses. *Bioinformatics* **23(5)**: 641–643.

- Yi, N., *Shriner, D.*, Banerjee, S., Mehta, T., Pomp, D., and Yandell, B. S. 2007. An efficient Bayesian model selection approach for interacting QTL models with many effects. *Genetics* **176**: 1865–1877.
- *Shriner, D.*, Vaughan, L. K., Padilla, M. A., and Tiwari, H. K. 2007. Problems with Genome-Wide Association Studies [Letter to the Editor]. *Science* **316(5833)**: 1840–1841.
- Liu, Y., McNevin, J., Zhao, H., Tebit, D. M., Troyer, R. M., McSweyn, M., Ghosh, A. K., *Shriner, D.*, Arts, E. J., McElrath, M. J., and Mullins, J. I. 2007. Evolution of human immunodeficiency virus type 1 cytotoxic T-lymphocyte epitopes: fitness-balanced escape. *J. Virol.* **81(22)**:12179–12188.
- Yi, N., and *Shriner, D*. 2008. Advances in Bayesian multiple QTL mapping in experimental crosses. *Heredity* **100(3)**:240–252.
- *Shriner, D.*, Baye, T. M., Padilla, M. A., Zhang, S., Vaughan, L. K., and Loraine, A. E. 2008. Commonality of Functional Annotation: a method for prioritization of candidate genes from genome-wide linkage studies. *Nucleic Acids Res*. **36(4)**:e26.
- *Shriner, D*. 2008. Putting Materials and Methods in Their Place [Letter to the Editor]. *Science* **322(5907)**:1463.
- Ankra-Badu, G. A., Pomp, D., *Shriner, D.*, Allison, D. B., and Yi, N. 2009. Genetic influences on growth and body composition in mice: multilocus interactions. *Int. J. Obes.* **33(1)**:89–95.
- *Shriner, D.*, and Yi, N. 2009. Deviance information criterion (DIC) in Bayesian multiple QTL mapping. *Comput. Stat. Data An.* **53(5)**:1850–1860.
- *Shriner, D.* 2009. Mapping multiple quantitative trait loci under Bayes error control. *Genet. Res.* In press.

Book Chapters
- Anderson, J. P., Rain, M., *Shriner, D.*, Rodrigo, A. G., Wang, Y., Nickle, D., Learn, G. H., Naugler, W. E., and Mullins, J. I. 2002. "The Genetics of HIV-1" in *The Human Immunodeficiency Virus: Biology, Immunology, and Therapy*, ed. Emini, E. A. (Princeton University Press, Princeton, NJ).
- *Shriner, D.*, Musani, S., and Yi, N. 2007. "Statistical methods for multiple QTL mapping in experimental crosses" in *Current Topics in Human Genetics: Studies of Complex Diseases*, eds. Deng, H.-W., Shen, H., Liu, Y., and Hu, H. (World Scientific Publishing Co. Pte. Ltd., Singapore).
- *Shriner, D.*, Coulibaly, I., Ankra-Badu, G., Baye, T. M., and Allison, D. B. "Genetic Contribution to the Development of Obesity" in *Understanding Obesity: Biological, Psychological and Cultural Influences*, eds. Akabas, S. R., Aronne, L. J., Nonas, C. A., Pi-Sunyer, F. X., and Wadden, T. A. (Wadsworth Publishers, Belmont, CA).

PROFESSIONAL ACTIVITIES
- 1995–2006, member of American Society for Microbiology
- 1997–present, member of American Association for the Advancement of Science
- 2006–present, member of The Obesity Society
- 2006–present, member of the American Statistical Association
- 2007–present, member of the American Society for Nutrition
- Invited Referee: Evolution, Journal of Leukocyte Biology, Journal of Molecular Evolution, Journal of Theoretical Biology, Molecular Biology and Evolution, Physiological Genomics, 2006 Computational Systems Bioinformatics Conference, Journal of the American Medical Association, Computational Statistics and Data Analysis, PLoS Computational Biology, American Journal of Human Genetics,

Molecular Ecology, International Journal of Immunogenetics, Molecular Phylogenetics and Evolution, BMC Genetics, Statistical Applications in Genetics and Molecular Biology, PLoS Genetics, Heredity, 2008 Computational Systems Bioinformatics Conference, Behavior Genetics

CONFERENCES

Posters

- 7th Annual HIV Dynamics and Evolution Conference, Seattle, WA, April 2000: "Inferring phylogenies for large, serially sampled data sets" and "Phylogenetic evidence for recombination within an HIV-1 singly infected individual"
- Joint Statistical Meetings, Seattle, WA, July 2006: "Inferring Quantitative Trait Loci Using a Bayesian Variable Selection Model and Markov Chain Monte Carlo Convergence Diagnostics"
- Annual Scientific Meeting of NAASO, The Obesity Society, New Orleans, LA, October 2007: "Commonality of Functional Annotation: A Method for Prioritization of Candidate Genes from Genome-Wide Linkage Studies"
- Genome-wide Association: *Analyze This!*, National Institutes of Health, Bethesda, MD, August 4–5, 2008: "Powerful, Flexible, and Efficient Multi-locus Genome-wide Association Testing Reveals Pathways Involved in Parkinson Disease"

Oral Presentations

- Annual Scientific Meeting of NAASO, The Obesity Society, Boston, MA, October 2006: "Bayesian Mapping of Obesity-related Quantitative Trait Loci in *Drosophila melanogaster*"
- 6th Annual Meeting of the Complex Traits Consortium, Braunschweig, Germany, May 26–29, 2007: "Bayes Error Control for Multiple QTL Mapping"

INVITED SEMINARS

- Section on Statistical Genetics Lecture Series, Department of Biostatistics, University of Alabama at Birmingham, December 6, 2006: "Bayes Error Control for Multiple QTL Mapping"
- University of Maryland Bioscience Day, November 13, 2007: "Developing a Comprehensive Research Toolkit"

HONORS AND AWARDS

- 1994–1995, Howard Hughes Medical Institute Undergraduate Research Fellow
- 1995–present, The Phi Beta Kappa Society
- 1995, P. Arne Hanson Award for the Outstanding Departmental Honors Student, Department of Microbiology, University of Maryland at College Park
- 1995, Honorable Mention, National Science Foundation Graduate Research Fellowship Program
- 1996, Honorable Mention, National Science Foundation Graduate Research Fellowship Program
- 1996–2001, Howard Hughes Medical Institute Predoctoral Fellow in Biological Sciences
- 2006, Finalist for the Ethan Sims Young Investigator Award, The Obesity Society
- Spring 2007, Career Enhancement Award, Office of Postdoctoral Education, University of Alabama at Birmingham

COMPUTER SKILLS
- Proficiency working under Mac, UNIX, and Windows operating systems
- Experience with C and Python programming languages
- Working knowledge of sequence analysis tools, such as CLUSTALW, DnaSP, LAMARC, MacClade, MEGA, PAML, PAUP*, Sequencher, TreeEdit, and TreeView
- Working knowledge of sequence simulation software, such as ms, Seq-Gen, and Treevolve
- Working knowledge of statistical analysis tools, such as JMP, Excel, Resampling Stats, R, and WinBUGS

REFERENCES
- David B. Allison, PhD, Department of Biostatistics, Section on Statistical Genetics, and Clinical Nutrition Research Center, Department of Nutrition Sciences, University of Alabama at Birmingham, Birmingham, AL 35294, Tel: +1 (205) 975-9167, E-mail: dallison@uab.edu
- Hemant K. Tiwari, PhD, Department of Biostatistics, Section on Statistical Genetics, University of Alabama at Birmingham, Birmingham, AL 35294, Tel: +1 (205) 934-4907, E-mail: htiwari@uab.edu
- Nengjun Yi, PhD, Department of Biostatistics, Section on Statistical Genetics, University of Alabama at Birmingham, Birmingham, AL 35294, Tel: +1 (205) 934-4924, E-mail: nyi@ms.soph.uab.edu
- Charles Rotimi, PhD, Center for Research on Genomics and Global Health, National Institutes of Health, Bethesda, MD 20892, Tel: +1 (301) 451-2303, E-mail: rotimic@mail.nih.gov